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**Lab: Using Online Molecular Databases to Study Evolutionary Relationships**

Ms. OK, AP Biology, 2014-2015

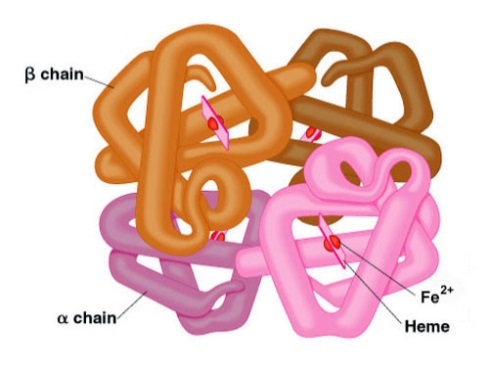
**Background Information:**

How does an evolutionary biologist decide how closely related two different species are? The simplest way is to compare the physical features of the species (their “morphologies”). This method is very similar to comparing two people to determine how closely related they are. We generally expect that brothers and sisters will look more similar to each other than two cousins might. If you make a family tree, you find that brothers and sisters share a common parent, but you must look harder at the tree to find which ancestor the two cousins share. Cousins do not share the same parents; rather, they share some of the same grandparents. In other words, the common ancestor of two brothers is more recent (their parents) than the common ancestor of two cousins (their grandparents), and in an evolutionary sense, this is why we say that two brothers are more closely related than two cousins.

Similarly, evolutionary biologists might compare salamanders and frogs and salamanders and fish. More physical features are shared between frogs and salamanders than between frogs and fish, and an evolutionary biologist might use this information to infer that frogs and salamanders had a more recent common ancestor than did frogs and fish.

This methodology certainly has problems. Two very similar looking people are not necessarily related, and two species that have similar features also may *not* be closely related. Comparing morphology can also be difficult if it is hard to find sufficient morphological characteristics to compare. Imagine that you were responsible for determining which two of three salamander species were most closely related. What physical features would you compare? When you ran out of physical features, is there anything else you could compare? Many biologists turn next to comparing genes and proteins. Genes and proteins are not necessarily better than morphological features except in the sense that differences in morphology can be a result of environmental conditions rather than genetics, and differences in genes are definitely genetic. Also, there are sometimes more molecules to compare than physical features.

In the following exercise, you will use data in a public protein database of gene products (proteins) to evaluate evolutionary relationships. In the **first part** of the exercise, you will be creating a phylogenetic tree for a group of organisms based on morphological characteristics only. In the **second part** of the exercise, you will use an online database to generate a phylogenetic tree for the same groups of organisms using protein sequences..

[](http://www.google.com/url?sa=i&rct=j&q=&esrc=s&frm=1&source=images&cd=&cad=rja&docid=IUHRREM5PBuOJM&tbnid=oKsgdeSkoAPFeM:&ved=0CAUQjRw&url=http://themedicalbiochemistrypage.org/hemoglobin-myoglobin.php&ei=R6U5UqztBsnc4AOIqYGAAQ&bvm=bv.52288139,d.dmg&psig=AFQjCNEpnPvIa0mc56naiQknDy3_JOvTYg&ust=1379595970502240)

You will obtain your data from a public online database that contains the amino-acid sequences of proteins coded for by many genes for many different organisms. Hemoglobin, the molecule that carries oxygen in our bloodstream, is composed of four subunits. In adult hemoglobin, two of these subunits are identical and coded for by the alpha hemoglobin gene. The other two are identical and coded for by the beta-hemoglobin genes. The hemoglobin genes are worthy of study themselves, but today we will just use the protein sequences as a set of traits to compare among species.

**Part One: Determining Relationships Among Groups of Vertebrates Using Morphologies**

In this part of the lab, you will view several examples of vertebrate organisms and determine what characteristics they have in common with one another. (*Note: vertebrates are organisms with a backbone and spinal cord).* You will also make a note of what characteristics distinguish them from one another. To do this, fill in the chart given below.

|  |  |  |
| --- | --- | --- |
| **Species Name** | **Similarity Shared with at Least One Organism in the List**  (provide one and identify the other organism) | **Difference From MOST Other Organisms on the List**  (provide one for each organism) |
| *Homo sapiens* (Human) |  |  |
| *Caretta caretta* (Loggerhead sea turtle) |  |  |
| *Branta canadensis (Canada goose)* |  |  |
| *Canis familiaris (*Dog) |  |  |
| *Balaenoptera acutorostrata* (Common minke whale) |  |  |
| *Heterodontus portusjacksoni* (Port Jackson shark) |  |  |

Using the morphological similarities and differences you recorded on the previous page, draw a phylogenetic tree where each “branch” represents one of your organisms. Ms. OK will provide an example of the basic structure for your phylogenetic tree. Organisms that are close together on the tree should be more closely related than organisms that are far apart on the tree. (*Note: Your answers do not need to be “perfect.” However, they must show an understanding of the connection between morphological similarity and increased evolutionary relatedness.)*

**Phylogenetic Tree Based on Morphological Characteristics**

**Part Two: Determining Relationships Among Groups of Vertebrates Using Molecular Data for a Known Protein Sequence**

1. Now you will use a publicly available database known as Uniprot to find molecular information about each of these organisms. Go to the following website: <http://www.uniprot.org>.
2. For this activity, you will search in the database for information about the hemoglobin beta protein. Hemoglobin beta is a subunit of the hemoglobin protein, an oxygen carrying pigment with four subunits found on red blood cells. In the search bar at the top, type in “Hemoglobin beta.”
3. Use keystroke “Control F” and the names of the organisms to find the protein “Hemoglobin subunit beta” for each of the six organisms out of the list of proteins given. Check the box to the left of each organism. Once you have done so, hit the “Align” button above the list.
4. Once the program has aligned the sequences, click “Tree” under the “Display” heading.
5. Copy the phylogenetic tree given in the space below. Write the common name of each organism at the end of the branches instead of the abbreviated scientific name given by the program.

**Phylogenetic Tree Based on Amino Acid Sequences:**

**Discussion Paragraph:**

In your discussion paragraph, please include the following information.

1. Describe the evidence used to create your phylogenetic tree based on morphology. What similarities did you use to place certain organisms close together, and what differences did you use to place certain organisms far apart? Describe at least three pieces of evidence.
2. State whether your two phylogenetic trees (one based on morphology and the other based on molecular evidence) were the same or different. If different, please identify exactly how they are different.
3. Identify the evidence that you find to be most accurate in creating phylogenetic trees—morphological or molecular. Explain your reasoning by answering the following question: Do all morphological similarities result from evolutionary relatedness? You should define and use the following terms in your response—homologous and analogous structures.

**Rubric:**

The following rubric will be used to evaluate your discussion paragraph.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Category** | **You Got It!**  (3 points) | **You’re Almost There!**  (2 points) | **You Need to Make Some Changes!**  (1 point) | **Your Score** |
| Part A | You directly connected at least three pieces of morphological evidence (similarities AND differences) to the groupings of organisms shown on your phylogenetic tree. | You included less than three pieces of evidence, you discussed either similarities or differences, or your connection between the evidence and your phylogenetic tree was somewhat unclear. | You included insufficient evidence and did not show a logical connection between the evidence and your phylogenetic tree. | /3 |
| Part B | You clearly stated whether your two phylogenetic trees were identical or different and you identified specific differences if applicable. | Your statement of whether your two phylogenetic trees were identical or different was slightly unclear or you identified some (but not all) differences or your differences were not specific enough. | You did not state whether your two phylogenetic trees were identical or different or you did not identify any differences between your trees (if applicable) | /3 |
| Part C | You correctly identified the type of evidence that is most accurate (morphological or molecular). You clearly supported this claim by defining and discussing the terms “homologous” and “analogous” structures. | You correctly identified the type of evidence that is most accurate but your support of this claim with the terms homologous and analogous structures lacked thoroughness or accuracy. | You did not correctly identify the type of evidence that is most accurate and you did not correctly include the terms homologous and analogous structures in your explanation. | /3 |